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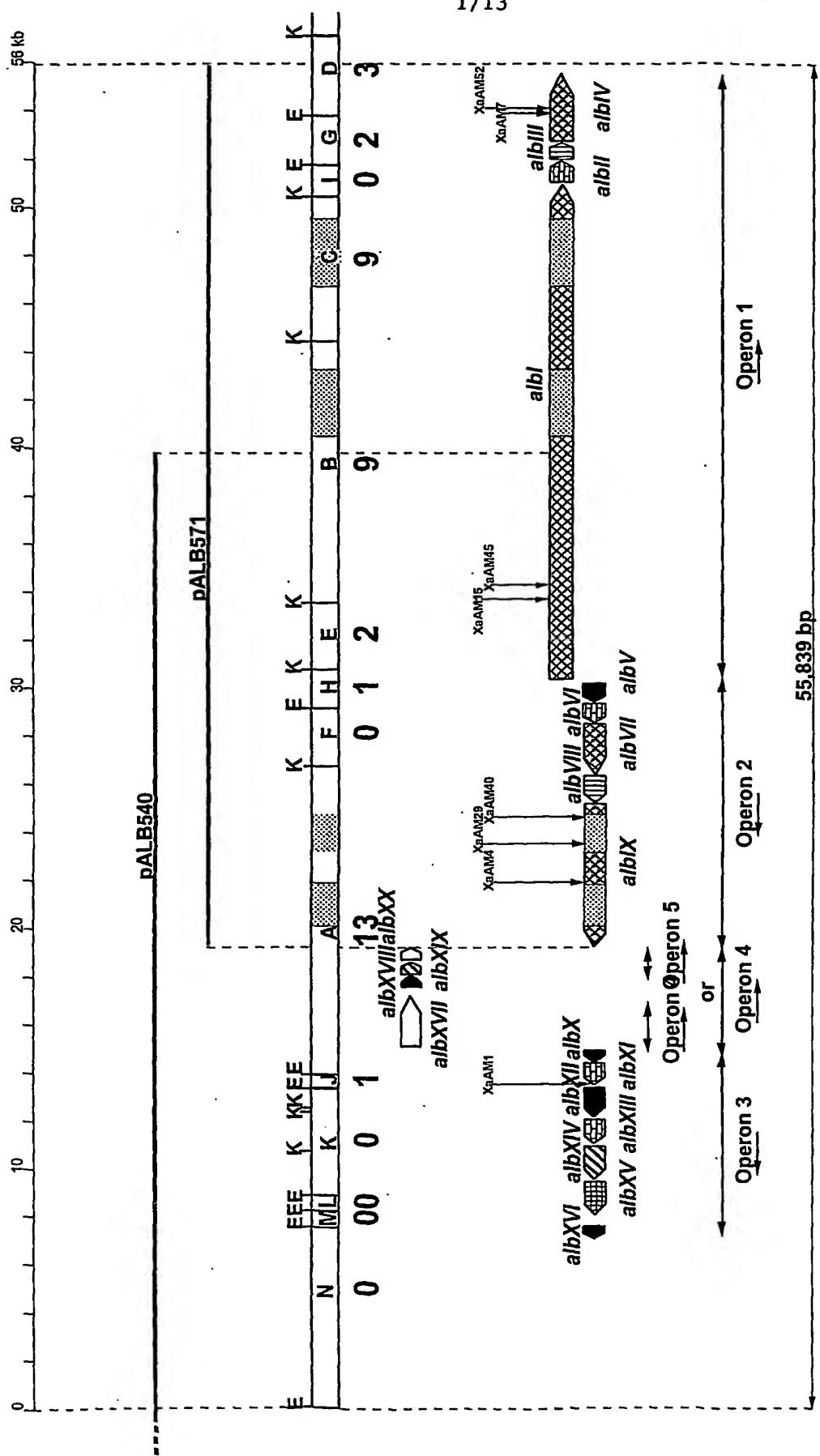
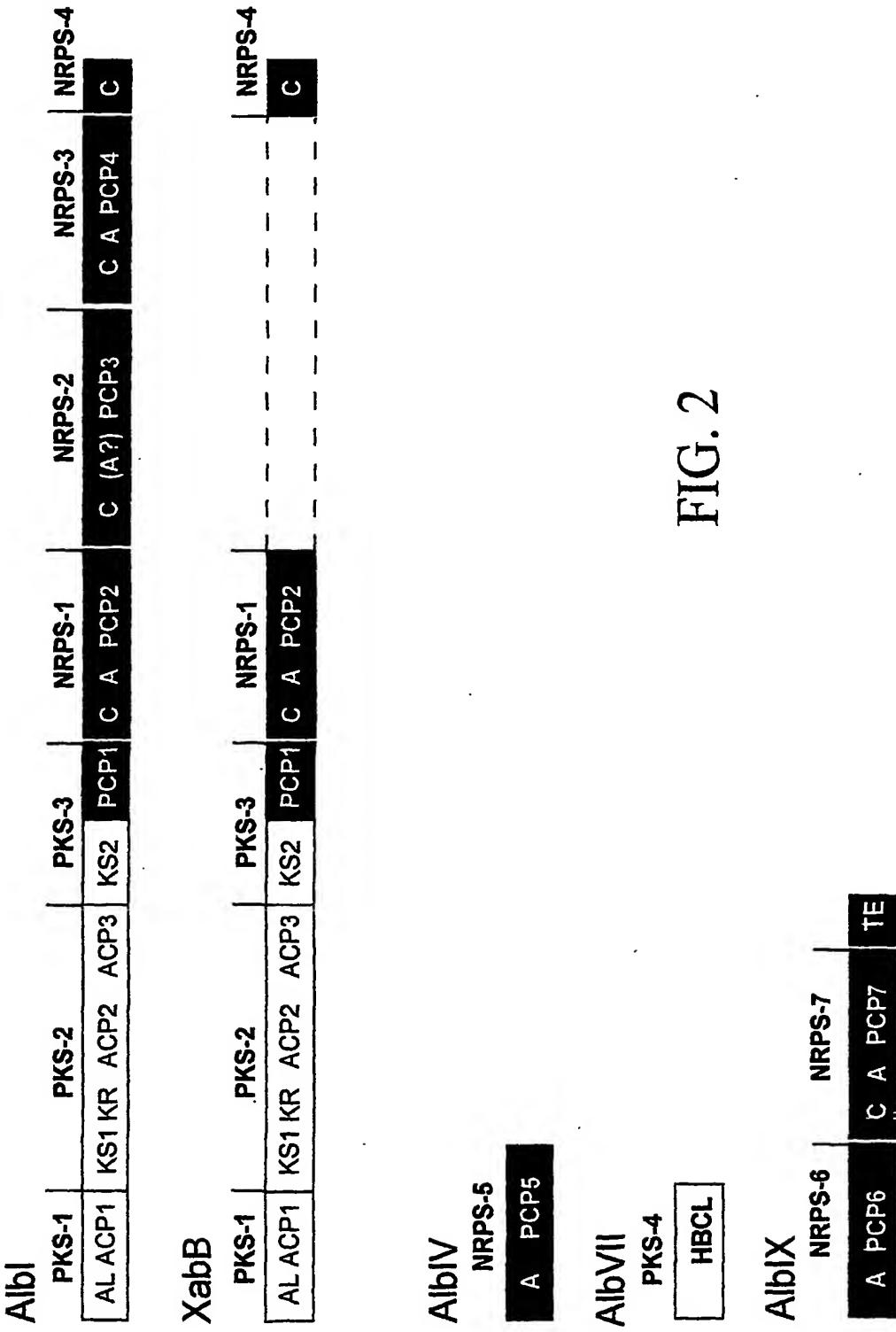


FIG. 1

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Sgl-TcmO	173	FVDLGGARG	234	PRADVFTV	263
Sgl-TcmN	331	IADLGGGDG	393	TGYDAYLF	423
Smy-MdmC	64	VLEIGTFTG	135	GAFDIVEV	159
Mxa-SafC	63	TLEVGVFTG	134	GTFDLAFI	158
Ser-EryG	85	VLDVGFGLG	149	ETEDRVTG	178
Spe-DauK	183	VLDVGGKG	254	RKADAILL	273
Sal-DmpM	208	VVDIGGADG	269	GGGDLYVL	298
Shy-RapM	106	VLEVGGCMG	155	VQGDAEEL	194
Sav-AveD	71	VLDVGGSG	124	GSFDAAWA	151
Sar-Cmet	158	VLDVACGHG	220	GPYDLSLI	251
AlbII	174	VLDVAAUGHG	236	SGYDVILL	267
		Motif I		Motif II	
		Motif III		Motif III	Motif IV

FIG. 3

Sgl-tcmP	84	VVLHLACGLDSRAFRMDVFD109	DVDVFDVIELR	139	EDWLDTVP
Sme-PKS	84	TVLHLGCGLDSRIFR1DGP109	ELDVPDVISLR	139	RGWIERLP
Pmu-tcmP	86	VVVQLGAGLDARFERLKGKPQ111	DLDLPEVINIR	141	TDWMKTVS
Mtu-Omt	85	TVVALLAEGLQTSFWRLDVAI113	TVDLPPFDLRL	144	YSWMDSVD
Mlo-Hp	84	IVLHLGCGLDTRVFRVDPFP109	DADYPQVIELR	139	PGWLAEV
Mtu-Hp	101	QVALLASGLDSRAYRLPWP127	EIDQPKVMEFK	162	ADWPITALQ
Mtu-Hp2	104	QVVILLASGLDSRAYRLPWP129	EIDQPKVLEFK	162	QDWPKALQ
Mtu-Hp3	98	QVVILLAGLDSRAYRLPWP123	EIDRPQVLDFK	156	DDWPQALR
Mtu-Hp4	101	QAVVVAAGLDCRAYRLDWQD126	EIDVPKVLEFK	161	TDWPPTPLT
Sco-Hp	93	QVVILLAGMDSRAFRMAWPE118	EVDTPALEEFK	153	EDWPSALA
AlbVI	99	QVVILLAGMDRAYRLPWPS124	EIDHMDVLSDK	157	EDWQALK
		Motif I	Motif II	Motif III	Motif IV

FIG. 4

FIG. 5

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XALB1 Strand +	29 bp downstream from the TGA stop codon of <i>abbXVII</i>	-40 -35 -30 -25 -20 -15 -10 -5 -1+ +5	P	S

17085=>	ACCATTGTGAACGGCCCTCCGGCTTCGTCCATAGCGATTTCGATCGGGGC	4.30	0	
	-----	-----	-----	
XALB1 Strand +	400 bp downstream from the TAA stop codon of <i>abbIV</i>	-40 -35 -30 -25 -20 -15 -10 -5 -1+ +5	P	S

55617=>	CATGGCTGCAGGCCGAGCTCGCTCAGCTACGGGTGAGAACCGAAGCTGCC <= 55667	4.13	12	
	-----	-----	-----	
XALB1 Strand -	62 bp, 170 bp and 560 bp downstream from the TAG stop codon of <i>abbXVII</i>	-40 -35 -30 -25 -20 -15 -10 -5 -1+ +5	P	S

7030=>	GGGGGGCAAGTTGCCCGGACCCCCGGTTCTGTAAACGTTGGCTGTCTGTAG <= 6879	3.95	13	
	-----	-----	-----	
	-----	-----	-----	
6922=>	AACTCTAAAAGAGATTGATTAAATTCCCTGCCTTTTGTACCGAGAATA <= 6872	4.42	0	
6532=>	TACTTAATAAGATTGCGAAGCTTGCCTTGCGGAATGATTTCAAATAT <= 6482	4.27	53	
	-----	-----	-----	
XALB3 Strand +	-40 -35 -30 -25 -20 -15 -10 -5 -1+ +5	P	S	

- 8065=>	GCAAAGAAAAGCGGAAACGAAAAAAGGGCCTACGGGCCCTTTCTTCCA	4.78	0	
- 8072=>	AAAGCGGAAACGAAAAAAGGGCCATCGGGCCCTACGGGCCCTTTCTTCCA	3.94	86	
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FIG. 6

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14456 GTCGTTGATCAGCACCAGATAAGCCTGTTCCCTCGAACGTCATCCTAAAGATAACCCCGGAAGGCCAGCTGGAAAGCAACGGAAAGTTGCTACATCGCAC
CAGCAACTAGTGTGGCTATTGGACAAGGAGCTTGCAAGTAGGATTCTATGGGGCCTTCGGACGGCTTCGTTGCTACAGATGTAGCTGCTG
D N I L V L Y A Q E E F T M
RBS
albX

-35 (P_{albX}: operon 3) -10 (P_{albX}: operon 3)

14552 AATGGGATTCAGATGGACCAAGGAAAGCGACTATACATGACGTCACCTCGAAGATGTCAAGGAAATAAGCCGTGAAGAGGCCAGTAAGAGTGTATGT
TTACGCTTAAGTCTACCTGGTTCGCTGACTATGTAATGCTACAGTTCTACAGTTCTACGTTCTGCAACTCTCACTACA
-10 (P_{albXVII}: operon 4) -35 (P_{albXVII}: operon 4)

14648 GTTTCGCACCGCTGTACGTCCCCATCGCCCATCGCGCAAAAGCTTACACGAAAAAATTACCCAGGGCATGGCTCAATAAGCCAAATAATCC
CAAAGCGTGGCGACATGCAGGGTAGGGCTGGTTTCGAATGTGCTTAAAGTGGTCCCCGTACGCAAGTTATGCCCCAGTTTCGTTATAGG

14744 TTGGCCTTGCAGAGCTATGTTGCGTGAAGGCCAAGGCCAGTGGGGAGCAACACCTTGGTTGGGTAGGCAATTCTGCTTA
AACGCGAACAGTCTCGATAACAGCACGCAATTCCGGTTCCGTACCCCTCGTTGTGAAACCCAAGCCAACTCCAGCCCCATCGTTAAAGACGAAT

RBS
14840 ATATCCACGGCGGGGGTTTGTCTTGGCGGTCAACTGTCATCGAGCAAGTCTGGGAGGCTATTTGCGCTGCCTTATCATAAAATAATTAC
TATAGGTGGCGCCGGCAAAACAGAACGGCCCGCAAGTGCAGAGTAGCTCGTCAGACAGAGTAAACGCGACGGAAATAGTTTATATAATG
M R C L I I N N Y
albXVII

FIG. 7A

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17332 GAATGAGGCCAACCGGCTGCTGATGGATAACGGCCGGCTGGCTGGGAATCTGTTCCCTCG
CTTACTCCGGGGTGGGAATGGCGCTTGGCTGGCGACTACCTATGGCCGGCCACCAAGCTGGTGTAGACAAGGAGC

M R P P R I R A N Q D G L
albXVIII (non expressed ?)

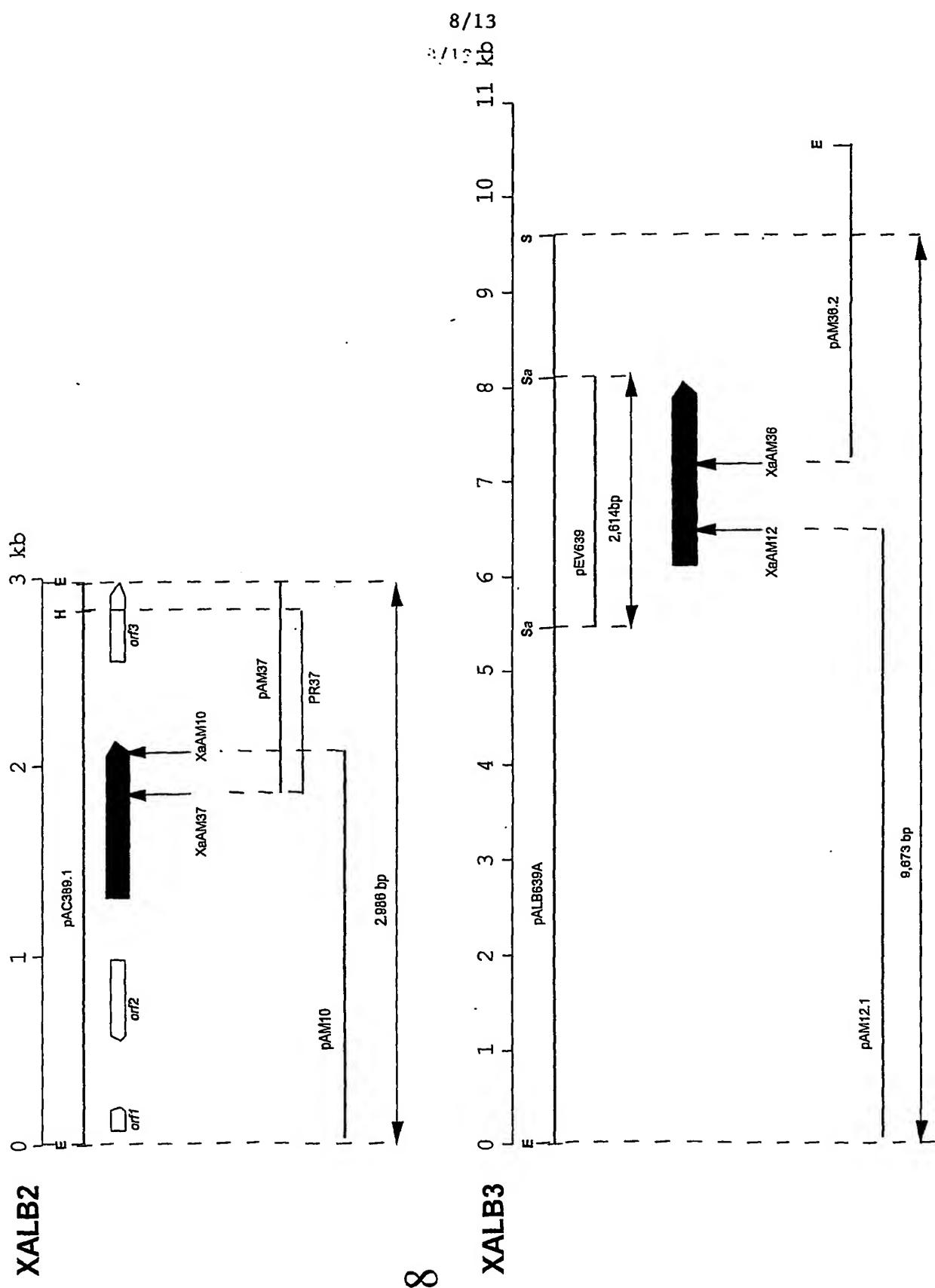
17428 TCGAGAACGGCCATCTGGTGAACGCCGACCTGGGGCTGGGGCTCAGGGGATCATGGAGGGCAGGGTGTATGGCCGGCAGCACGGTC
AGCTCTGCCGGTAGACCACTGGGGCTGGACCCGGACCCGGCAGTGGCCCTAGTACGCTCCACTAGCTTACCGGCCGTGTCAG
17524 TCGCCTGGCGGTAAAGCACGTCTATCCGGACCGCTAGTGGTGTCTAGGGAGGTGTTCTGACTAACGCCGTGTTGGCATCTGCTGGTGC
AGCGGACGCCATTCTGCAAGATAGGCCCTGGTGAACAGTGGCACAGTCCACAAAGACTGATGGCACAAAGCGTAAAGCACACGGCT
-35 (PalbXIX: operon 5) -10 (PalbXIX: operon 5)
17620 GCATTGACGCTCACAGCTACCGCATCGATCCCTGTTACCCCTGCGTTGCTCGATGCCCTGCTGATGGCGTATATTACCCGAAACGGTCACTACATC
CGTAACTGCGAGTGTGATGGCTAGCTAGGACAATGGGACAAACGAGCTACGGGACACAGTGGCTGCCAGTGATGTAG

RBS

17716 AGTTTCCACCCATGCCGGCTAACGACCCCTGCTGAAAGCAAGGATTACTGTGGAGAAAGCTTCTGTCAGGGAAGATCGCTCCGGCAATCGCTGGAGTCG
TCCAAAGGTGGTACGGCGGGTACTGGGAAACTTCTGGTCCATAATGACACCTCTTCGAAGCAGTGGCTCTAGGAGGGCCGGTAGCGAACCTCAGC

M P A K L E S K D Y C G E S F V S
albXIX

FIG. 7B



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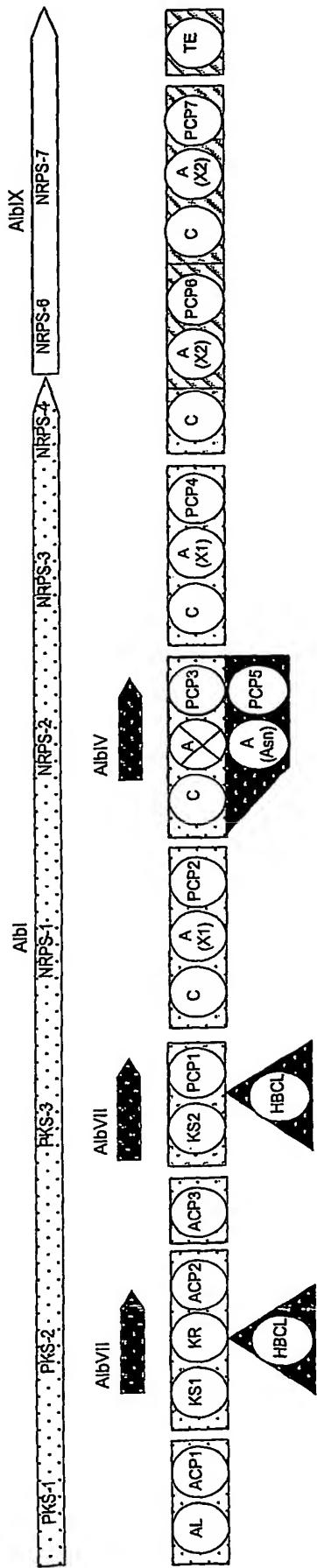


FIG. 9A

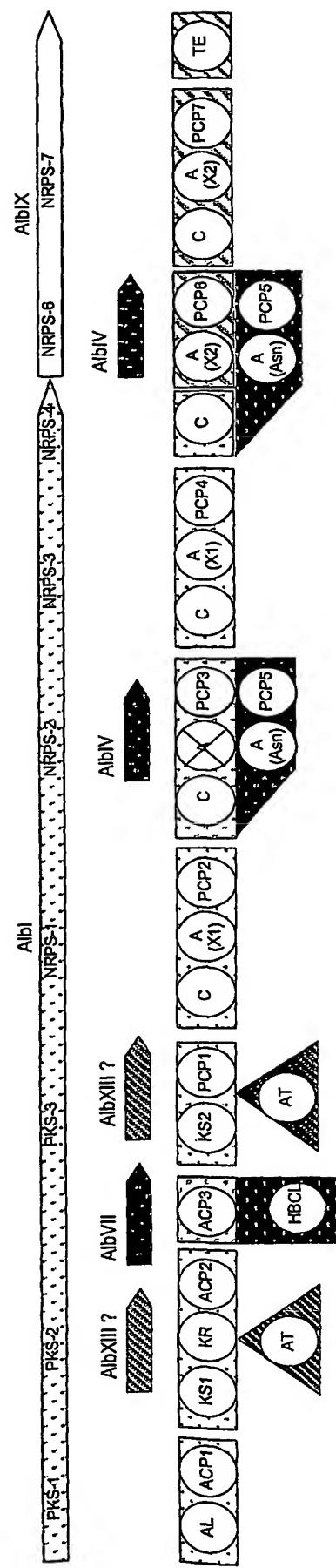


FIG. 9B

Ri fA-1 LGRVDVLOPACFAVMVGLAAVWESVGVRPDAVVGHSQGEI
Ri fA-2 LDQTMYTQGALFAVETALFRLFESMGVRPGLLAGHSIGEL
Ri fA-3 LDRVDVQQPASEFAMMVGLAAVWTSLGVTpDAVLGHHSQGEI
Ri fB-1 LDRVDVQQPASEFAMMVGLAAVWEVGVRPDAVVGHSQGEI
Ri fE-1 LNQTVFTGAGLFAVESALERLAESWGVRPDVVLGHHSIGEI
BlmVIII ADDTRAQOPALFAVEYYALARTLMDGVVRPAAMLGHSIGEV

FIG. 10A

AlbXIII LEDRPRHIRAVIDLTGHAQFGPAIQAHNVAVIGHSVGGY
FenF TRTMNAQPAILTVSVTIAQVYMQEIGIKPHFLAGHSLGEGY
LipA PDSRGRQLLAAALDYLTGRSSVRGRIDSRLGVMGHSMGGG

FIG. 10B

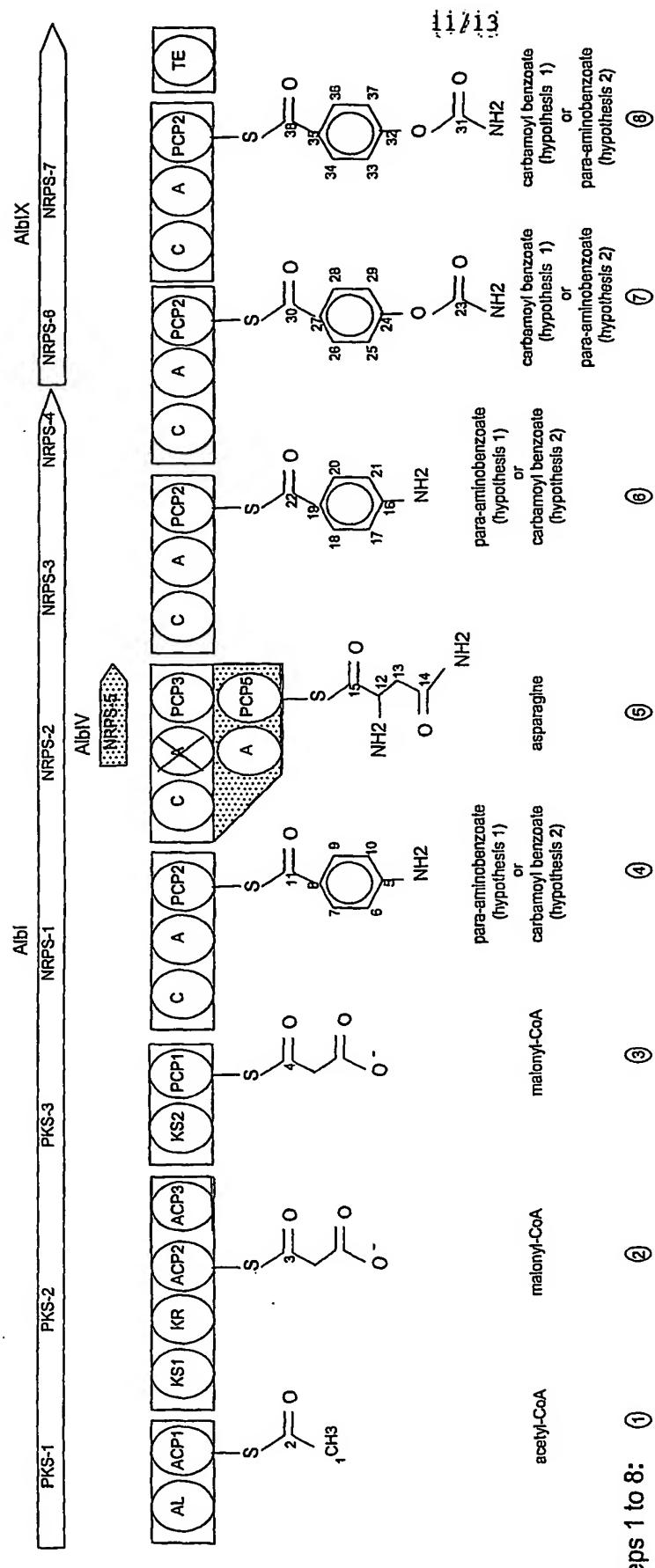


FIG. 11A

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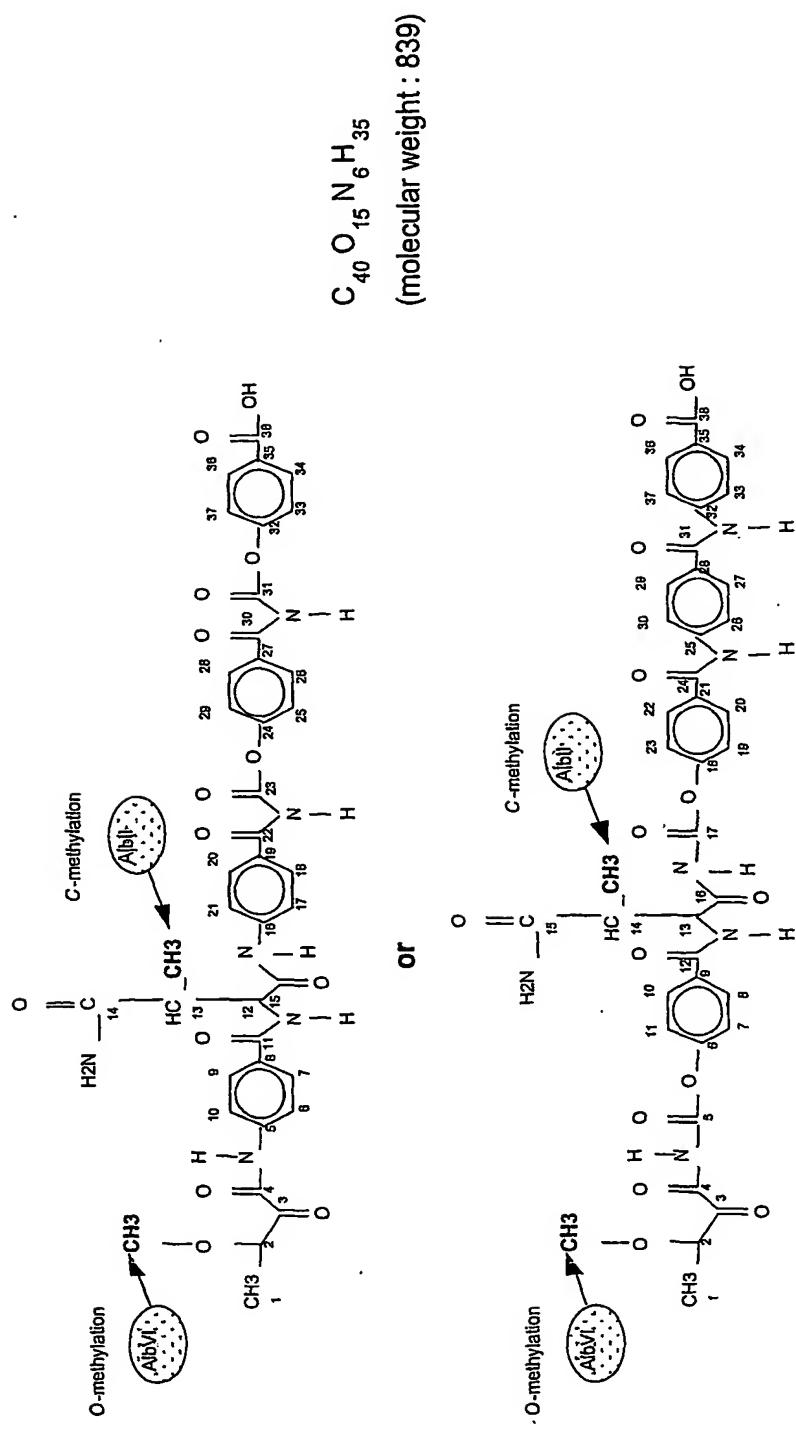


FIG. 11B

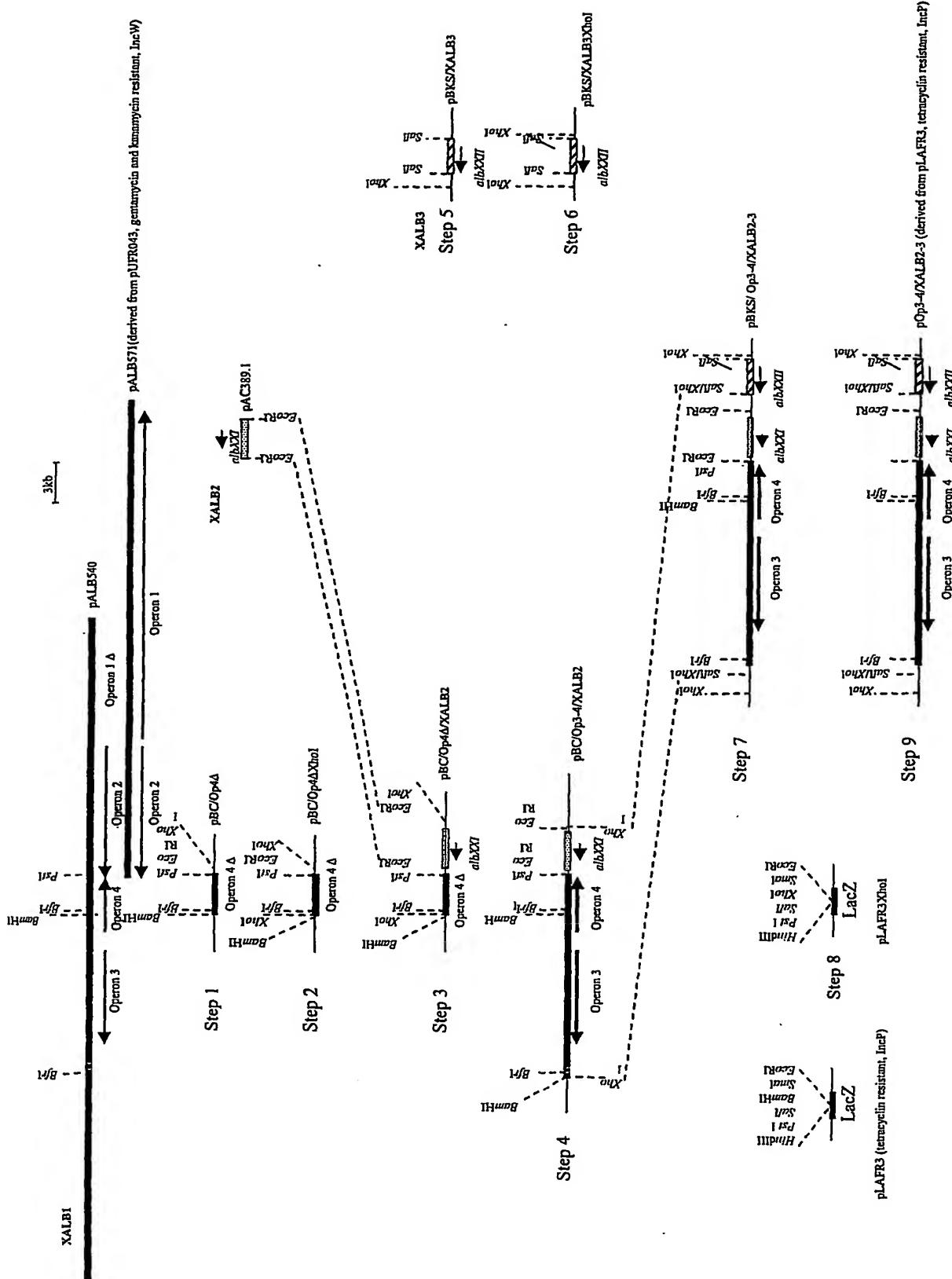


FIG. 12